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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/165,460	10/02/1998	JASPER D. RINE	B96-021-3	7914

23379 7590 02/21/2002

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HILLSBOROUGH, CA 94010

EXAMINER

RAMIREZ, DELIA M

ART UNIT	PAPER NUMBER
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1652

DATE MAILED: 02/21/2002

20

Please find below and/or attached an Office communication concerning this application or proceeding.

Advisory Action

Application No.

09/165,460

Applicant(s)

RINE ET AL.

Examiner

Delia M. Ramirez

Art Unit

1652

--Th MAILING DATE of this communication appears on the cover sheet with the correspondence address --

THE REPLY FILED 24 January 2002 FAILS TO PLACE THIS APPLICATION IN CONDITION FOR ALLOWANCE. Therefore, further action by the applicant is required to avoid abandonment of this application. A proper reply to a final rejection under 37 CFR 1.113 may only be either: (1) a timely filed amendment which places the application in condition for allowance; (2) a timely filed Notice of Appeal (with appeal fee); or (3) a timely filed Request for Continued Examination (RCE) in compliance with 37 CFR 1.114.

PERIOD FOR REPLY [check either a) or b)]

- a) ☒ The period for reply expires 3 months from the mailing date of the final rejection.
- b) ☐ The period for reply expires on: (1) the mailing date of this Advisory Action, or (2) the date set forth in the final rejection, whichever is later. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of the final rejection. ONLY CHECK THIS BOX WHEN THE FIRST REPLY WAS FILED WITHIN TWO MONTHS OF THE FINAL REJECTION. See MPEP 706.07(f).

Extensions of time may be obtained under 37 CFR 1.136(a). The date on which the petition under 37 CFR 1.136(a) and the appropriate extension fee have been filed is the date for purposes of determining the period of extension and the corresponding amount of the fee. The appropriate extension fee under 37 CFR 1.17(a) is calculated from: (1) the expiration date of the shortened statutory period for reply originally set in the final Office action; or (2) as set forth in (b) above, if checked. Any reply received by the Office later than three months after the mailing date of the final rejection, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

1. ☐ A Notice of Appeal was filed on _____. Appellant's Brief must be filed within the period set forth in 37 CFR 1.192(a), or any extension thereof (37 CFR 1.191(d)), to avoid dismissal of the appeal.
2. ☐ The proposed amendment(s) will not be entered because:
- (a) ☐ they raise new issues that would require further consideration and/or search (see NOTE below);
 - (b) ☐ they raise the issue of new matter (see Note below);
 - (c) ☐ they are not deemed to place the application in better form for appeal by materially reducing or simplifying the issues for appeal; and/or
 - (d) ☐ they present additional claims without canceling a corresponding number of finally rejected claims.

NOTE: _____

3. ☐ Applicant's reply has overcome the following rejection(s): _____.
4. ☐ Newly proposed or amended claim(s) _____ would be allowable if submitted in a separate, timely filed amendment canceling the non-allowable claim(s).
5. ☐ The a) ☐ affidavit, b) ☐ exhibit, or c) ☒ request for reconsideration has been considered but does NOT place the application in condition for allowance because: see attachment.
6. ☐ The affidavit or exhibit will NOT be considered because it is not directed SOLELY to issues which were newly raised by the Examiner in the final rejection.
7. ☒ For purposes of Appeal, the proposed amendment(s) a) ☐ will not be entered or b) ☒ will be entered and an explanation of how the new or amended claims would be rejected is provided below or appended.

The status of the claim(s) is (or will be) as follows:

Claim(s) allowed: none.

Claim(s) objected to: _____.

Claim(s) rejected: 31, 33-35, 37-39, 41-43, 45-46.

Claim(s) withdrawn from consideration: _____.

8. ☐ The proposed drawing correction filed on _____ is a) ☐ approved or b) ☐ disapproved by the Examiner.
9. ☐ Note the attached Information Disclosure Statement(s) (PTO-1449) Paper No(s). _____.
10. ☒ Other: see attached references

ADVISORY ACTION

1. Claims 31, 33-35, 37-39, 41-43, and 45-46 are pending in the application.
2. Applicants allege in the amendment filed in Paper No. 19, filed 1/24/2002, that the 103(a) rejection applied to claims 31, 33-34 and 41-42 over Rose et al. (GenBank accession number Z49617) in view of Nozaki et al. (US Patent No. 4,997,767) and the 103(a) rejection applied to claims 35, 37-38, 43, 45-46 over Lye et al. (GenBank accession number Z49260) are not in compliance with the notice requirement of 35 U.S.C. 132. According to the records of the instant application, two Notices of References Cited (PTO-892) have been sent to Applicant in Paper No. 11, mailed on 9/13/2000, and in Paper No. 16, mailed 3/27/2001, indicating that the cited references were sent to Applicant by the previous Examiner of record. Also, according to the records of the instant application, the reasons for applying said rejections have been extensively discussed in the previous Office Actions. In any event, copies of the Rose et al. and Lye et al. references (alignments) are being forwarded to Applicants with this action.
3. Applicants argue that the creation dates relied on by the Examiner to determine the public availability of Rose et al. (GenBank accession number Z49617, October 6, 1995) and Lye et al. (GenBank accession number Z49260, May 16, 1995) are not the dates when such references were available to the public. After communications with representatives of GenBank and EMBL, which is the database where these sequences were originally filed, it was indicated that the creation dates are the dates when these entries first become available to the public. According to their records, the creation dates for entries Z49617 and Z49260 are October 6, 1995 and May 16, 1995. Therefore, these references are considered valid prior art over Applicant's earliest priority date of August 7, 1996.

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4. In regard to the 103(a) rejection of claims 31, 33-34, and 39, 41-42, which is discussed in previous Office Actions, Applicants argue that while the entire yeast genome had been largely sequenced at the time the invention was made and open reading frames were identified, the claimed compositions would be neither anticipated nor obvious. Applicants further argue that the instant invention requires the coding sequence to be operatively joined to a promoter and that there was no motivation to select an open reading frame of unknown function, link it to an operative promoter, and express it in a vector. These arguments have been fully considered but are not found persuasive because once an open reading frame is known, one of ordinary skill in the art is motivated to insert the open reading frame in a vector with an operably linked promoter in order to characterize the protein encoded by such open reading frame. The existence of many open reading frames of unknown function does not eliminate the motivation to insert the open reading frame sequence into a vector to characterize the protein. On the contrary, one of skill in the art is highly motivated to determine the function of proteins encoded by unknown open reading frames.

5. In regard to the 103(a) rejection of claims 35, 37-38 and 43, 45-46, which is discussed in previous Office Actions, Applicants argue that Lye discloses computer predictions of thousands of possible coding sequences and does not disclose any gene or gene product. Applicants also argue that the Examiner uses Applicant's own disclosure to select one of many *Saccharomyces* genes and to provide motivation to recombine it in an expression vector. Furthermore, Applicants argue that in the absence of any evidence for function, there would be no motivation to select out one of the thousands of yeast ORFs of unknown function. These arguments have been fully considered but are not found persuasive because once an open reading frame is known

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or even predicted, one of ordinary skill in the art is motivated to insert the open reading frame in a vector with an operably linked promoter in order to characterize the protein encoded by such open reading frame. The existence of many open reading frames of unknown function does not eliminate the motivation to insert the open reading frame sequence into a vector to characterize the protein. On the contrary, one of skill in the art is highly motivated to determine the function of proteins encoded by unknown open reading frames. Constructing a vector comprising the polynucleotide of SEQ ID NO: 3 or a vector comprising a polynucleotide which will hybridize under stringent conditions to SEQ ID NO: 3, and transforming a host cell to express the corresponding protein would have been obvious to one of skill in the art at the time the invention was made once it was known that said sequence was an open reading frame. In response to Applicant's argument that the Examiner's conclusion of obviousness is based upon Applicant's disclosure, it must be recognized that any judgment on obviousness is in a sense necessarily a reconstruction based upon hindsight reasoning. But so long as it takes into account only knowledge which was within the level of ordinary skill at the time the invention was made, and does not include knowledge gleaned only from Applicant's disclosure, such reconstruction is proper. See *In re McLaughlin*, 443 F.2d 1392, 170 USPQ 209 (CCPA 1971). Moreover, the motivation disclosed in Applicant's disclosure is not the same motivation provided by the Examiner.

6. The request for consideration is acknowledged. The amendment filed on 1/24/2002 under 37 CFR 1.116 in reply to the final rejection has been considered but is not deemed to place the application in condition for allowance. For Appeal purposes, the status of the pending claims is as follows:

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Claims allowed: NONE

Claims rejected: 31, 33-35, 37-39, 41-43, 45-46

Claims objected: NONE

7. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (703) 306-0288.

The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (703) 308-3804. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

DR
February 15, 2002

Delia M. Ramirez, Ph.D.
Patent Examiner
Art Unit 1652



PONNATHAPU ACHUTAMURTHY
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2002, 13:20:11 ; Search time 4622.84 Seconds
(without alignments)
10520.305 Million cell updates/sec

Title: US-09-165-460A-3
Perfect score: 2948
Sequence: 1 tgaactgttgatgaacaaag.....ggggaggaataagaatcaca 2948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 824859755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
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16: em_fun:*
17: em_hum:*
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30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
C 1	2948	100.0	29987	8	SC8156	249260 S.cerevisiae
2	1560.4	52.9	4156	8	D50276	D50276 Saccharomyces
3	1361	46.2	4130	8	YSCNCR1G	L42821 Saccharomyces
4	1163	39.5	4225	8	SCD65682	U65682 Saccharomyces
5	1069.4	36.3	3250	8	SCU32580	U32580 Saccharomyces
6	931	31.6	3525	8	SCD63849	U63849 Saccharomyces
7	786.8	26.7	3240	8	YSCBUL1	D50083 Yeast BUL1
8	703.8	23.9	3020	8	SCRDS1GEN	X88901 S.cerevisiae
9	225.2	7.6	270	8	YSCGENC58X	M87379 Yeast Eco
10	143.8	4.9	27559	8	SC8339	Z49210 S.cerevisiae
C 11	75	2.5	2023	8	SCYNR068C	Z71683 S.cerevisiae
12	71.8	2.4	4775	8	SCU32938	U32938 Saccharomyces
C 13	68	2.3	780	11	CNS06K8B	AL402561 T7 and
14	65.6	2.2	256172	2	AC005139	AC005139 Plasmodium
15	65.6	2.2	310779	2	AC005140	AC005140 Plasmodium
16	64.4	2.2	904	11	CNS06I89	AL39967 T3 and
17	64.4	2.2	86827	3	PFMAL3P5	AL034536 Plasmodium
18	63.4	2.2	1920	3	PFCTUB	X62393 P.f. vari
19	63.4	2.2	110000	2	PFMAL13P2_0	AL049185 Pl. di
20	62	2.1	253305	3	PFMAL13P7	AL034559 Plasmodium
C 21	61.6	2.1	1141	6	AX083744	AX083744 Sequence
22	60.8	2.1	234112	3	PFMAL4P2	AL035475 Plasmodium
23	60.6	2.1	202872	2	AC016160	AC016160 Homo sap
C 24	60	2.0	5632	3	AF310892	AF310892 Dictyost
C 25	59.4	2.0	3214	3	AF019980	AF019980 Dictyost
26	59.4	2.0	318221	2	PFMAL13P3	AL049184 Plasmodium
27	58.8	2.0	321003	2	PFMAL4P3	AL035476 Plasmodium
28	58.4	2.0	78439	17	HS055197	HS055197 Homo sapie
C 29	58.4	2.0	169546	2	AC004157	AC004157 Plasmodium
30	58.4	2.0	245802	2	AC006279	AC006279 Plasmodium
C 31	58.4	2.0	251124	9	HUAE000660	AE000660 Homo sap
C 32	58.2	2.0	153098	3	PFMAL3P2	AL034558 Plasmodium
33	58	2.0	169794	2	AC004688	AC004688 Plasmodium
34	58	2.0	178137	2	AC011302	AC011302 Homo sap
C 35	57.8	2.0	13684	3	AE001403	AE001403 Plasmodium
36	57.8	2.0	153477	2	AC006278	AC006278 Plasmodium
C 37	57.6	2.0	53932	2	AC023371	AC023371 Homo sap
C 38	57	1.9	12029	3	AE001431	AE001431 Plasmodium
39	57	1.9	163443	2	AC006280	AC006280 Plasmodium
C 40	57	1.9	178273	2	AC005308	AC005308 Plasmodium
C 41	57	1.9	196149	2	AC004709	AC004709 Plasmodium
C 42	56.8	1.9	67970	3	PFMAL1P3	AL031746 Plasmodium
C 43	56.8	1.9	149627	9	AC087428	AC087428 Homo sap
C 44	56.6	1.9	92633	2	PFMAL4P1_3	Continuation (4 of
C 45	56.6	1.9	153477	2	AC006278	AC006278 Plasmodium

ALIGNMENTS

RESULT 1

LOCUS SC8156 29987 bp DNA PLN 11-AUG-1997
DEFINITION S.cerevisiae chromosome XIII cosmid 8156.
ACCESSION Z49260 Z71257
VERSION Z49260.1 GI:809081
KEYWORDS BUL1; cytochrome b5; DAG1; initiation factor 1A; inorganic pyrophosphatase; IPP2; nitrate reductase; orotate phosphoribosyltransferase; tau element; TIF11; TP53; transfer RNA-Gln; trehalose-phosphate synthase; U6 snRNP; URAL0.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 29987)
AUTHORS Lye, G. and Churcher, C.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 29987)
AUTHORS Barrell, B. and Rajandream, M.A.
TITLE Direct Submission

JOURNAL

Submitted (12-MAY-1995) *Saccharomyces cerevisiae* chromosome XIII
sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
CB10 1RQ E-mail: barriellesanger.ac.uk

COMMENT

Notes:
All CDS over 100 codons have been analysed. CDS that are completely
overlapped and those that are overlapped by more than 50%
of their length by a larger CDS have been omitted from this
analysis.
Details of the omitted CDS are available on request. The more
significant matches with motifs in the PROSITE database are
also included but some of these may be fortuitous. The length in
codons and the calculated codon adaptation index (CAI)
is given for each CDS.
Cosmid 8156 is overlapped at the start by cosmid 9920, emb1 entry
SC9920,

FEATURES

source

accession no. 248639 and at the end by cosmid 8021.

Location/Qualifiers

1. 29987
/organism="Saccharomyces cerevisiae"
/strain="AB972"
/db_xref="taxon:4932"
/chromosome="XIII"
/clone="cosmid 8156"
/map="13R"
complement(<1..356)
/note="YM8156.01c, unknown, len: 118, CAI: 0.14, overlaps
and extends YM9920.13c"

CDS

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/db_xref="SWISS-PROT:O03496"
/translation="MTDVFSSQIEFLRVKEFLIANNPAKINNENKDAVLTOIEHD
FYLQYKDGLPNLESRLFPDTSICLLRSQHIIASKIDSQELSAVKEQLLT
ENANIIIEYVLDFA"

misc_feature

1..140

/note="overlap with SC9920.248639 *S. cerevisiae* chromosome
XIII cosmid 9920"
complement(851..1312)
/gene="TIF1"
complement(851..1312)
/gene="TIF1"
/note="YM8156.02c TIF1 gene, IF1A_YEAST, P3891,
initiation factor 1a"
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/product="tif1p"
/protein_id="CAA89243.1"
/db_xref="GI:809083"
/db_xref="SWISS-PROT:P38912"
/translation="MGKNTKGGKRGKNDSDGPKRELIYKEGQGYAQITKMLGN
GRVEASCFDGNKMAHIGRLKRVWVGQDIIILSLRDFDQDCDYVHYKINLDEART
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complement(1678..4842)
/gene="TPS3"
complement(1678..4842)
/gene="TPS3"

gene

/note="YM8156.03c, TPS3 gene, len: 1054, CAI: 0.21,
SW.TPS3_YEAST P38426, alpha,alpha-trehalose-phosphate
synthase and PIR:S27471; PS00213 Lipocalin signature,
translation in TPS3_YEAST starts at amino acid 33 in this
sequence"

CDS

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/db_xref="SWISS-PROT:P38426"
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NNKQSSSVTSASHYIGLPQEAQINGEPLQRAVNSGATGVNHNEMLSQQFL
ELTANATAANGSIPRANPVSSGTAQRPVEFFSAPSVGSPQEAASISLA
SRSSAHNDLSSLKMLPNLSPDHPHVRSSSKAVITPVSKSPDVPDPAVYAKV
REEQOQASLP SHKRVSGSTAGDSSTASSSNLRYSOQFDNFIEDSEDSDSLE
TDATKYNVPKFGYSSNAKLASLRMSYELFKHLPITVDSDKNGSLKNAVNIAY
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OM

misc_feature

complement(2260..2301)
/gene="TPS3"

CDS

/note="PS00213 Lipocalin signature"
5199..6140
/note="YM8156.04, unknown, len: 313, CAI: 0.11, previous
noted ORF, SW:YTP3_YEAST P38430"
/codon_start=1
/product="unknown"
/protein_id="CAA89245.1"
/db_xref="GI:809085"
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/translation="MNLVDACHVITPDNTFCDDGSGQCLRCVMSNPNYDNN
KLAGRSKNDICVGFVHPYSHLFVGSRRKVSHYQDVLEYNEQFDSLVO
PEPDLLEYIKRENDTLVSGEIGLDKFLPANGFTMQNEKARLTATVVKLSH
TVFRFRLARHTSKPISHDVKCHGLNDICNEELLATYHSVKICLHSTVGSKEFLI
QMLKKFPDRIFVLSKWINFQDPEEGDALVRSPLSTCILTETDYPIDNPDFSYQK
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6392..6997

CDS

/note="YM8156.05, unknown, len: 301, CAI: 0.12,
SW:YTP2_YEAST P38429 previously noted ORF"
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/product="unknown"
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/db_xref="GI:809086"
/db_xref="SWISS-PROT:P38429"
/translation="MARPVNTAETSGRPTGGGYASNNNGSNNNGSNNNNNN
NNNNNNNNNGPTSSGRTNGKRLTAQOQYIKNLIEHTITDNRDPDKRSHH
DFEYTDALRYKDHQFDLPDNLTLQGLSLGKAKTYSYKRNTOGQHDKRIH
DLANVRRHDEHSIKETDCIPQFIYKVKKKKFKKEFRG"
7278..7889

CDS

/note="YM8156.06, unknown, len: 301, CAI: 0.13,
SW:YTP1_YEAST P38428, extends previously noted ORF"
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/product="unknown"
/protein_id="CAA89247.1"
/db_xref="GI:809087"
/db_xref="SWISS-PROT:P38428"
/translation="MEDSRLITLILVFGVIFLKKFFQSNQHPSAORLSAT.
PGSTQNALRRTRVNGGHPVTQVETVQNLAPNLHPQIYRISLENTGSVEIATV
LRGDEFSEPPGPRAPGANAADNNAAGGEFNDPKKMICAEMLDKFHDVLI
EDMSNLSFKDLIEERKLLVQAKNLETKLQSDKDLQSLLT"
complement(8013..9398)

CDS

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/product="unknown"
/protein_id="CAA89248.1"
/db_xref="GI:809088"
/db_xref="SWISS-PROT:Q03508"
/translation="HEEFEEFRKGMSSRCGNHRLVRKNWSCACELAVPFEVPEHAI
TKLHIYDNTLFTATPGTEQLYTRELLNLTSSLPNGMWRNPGFLQAALEISKT
PRYSWNADIVKLAESYSADTISVLTRGSESKFHLIEHALATQIRSHKWCSENEF
RFNAVCLAKRAISEYTSYKKELMRDELEYPSRELSDIRIDIRQIDAFKFFHSLD
LPRLKWSAIPVPFTKSPREQLEMDVMDVKNNSQALSTQKEDRLRTPQIGTIL
CTASHRLISIVIKLRKRRTRPKLIEHLYIPCAEPKQDPALEIAKVAWSND
TRTDSEKVOHISQIFLEQPGKIVFVTDLAVIASAHNRKRLVLPVPAPEI
NRYITFFKEFYIVTGHFKDRIEDLEVVTIERLINCKEDIEHWPLDITIPKAFGR
AKLAAPCSNA"
9991..12852

CDS

/note="YM8156.08, unknown, len: 953, CAI: 0.20, probable
integral membrane glycoprotein"
/codon_start=1

Query Match	100.0%;	Score 2948;	DB 8;	Length 29987;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2948;	Conservative	0;	Mismatches	0;	Indels
					0;
QY 1	tgaactgttgatgaacaaagagagagctgacaagcatcaaaagctttgtacgatgattccca	60			
Db	27785	TGAACGTGTTGATGAACAAGAGAGAGCTGACAGCATCAAAGCTTTGTACGATGATTCCA	27726		
QY 61	tccaadaatttggtaatatgaaccaggttccaacaagaatttcttgaataataatgagtt	120			
Db	27725	TTCAAAANTTTGTAATATGAACCACAGTTTCACACAGAAATTTCTTGAAATTAATGAGTT	27666		
QY 121	atataatatgaatatggggagacogtgggccaaaggaaactgaattttacagattttattac	180			
Db	27665	ATATAATATGAATAGGGAGACCGTAGGCCAAAGGAACGTAANTTTACAGATTTTATTAC	27606		
QY 181	ttcacagctgttttaacgatatcgaaagcatattgcaacttgaaagtttagttgttcacaactt	240			
Db	27605	TTCACAGCTGTTTAAAGCATATCGAAAGCATTTTGCACATTGAAAGTTAGTGTTCACAACCT	27546		
QY 241	atccaacattttaaaaaacaggctcagtcacccttaaacacacactcaaacagcagcattatc	300			
Db	27545	ATCCACACTTTTAAAAACAGCTCAGTACCCCTAAACACACACTCAAAAGCAGCATATTCT	27486		
QY 301	tgagattccaatatgcacacaggtgaacgggtagttcatcgtgcgccagttcagcgctcatt	360			
Db	27485	TGAGGATTCAATATCGCACACAGGTAAACGGTAGTTTCATCGTCCCCAGTTACGGTCAATT	27426		
QY 361	aacgcagtaacttcttcataccaagtagttatttttacctagcggtagctcgtctac	420			
Db	27425	AACGCCAGTAACCTTCTTCATCCAAGAGTAGTTATTATTTTAACTAGCGGTAGCTCGTCTAC	27366		
QY 421	ttcccttgaatttacagaccagatgttccataaaagggttagattgtctctttacagta	480			
Db	27365	TTCCCTGAAATTTACAGACCAGATGTTTCATAAATGGGTAGGATTTGGCTTTTACAGTA	27306		

Db 26225 GCCTTTTGGACTGGCAGCACACCATGCTATGAGCAATACAGGAAGCTCCAT 26166
QY 1621 gacaaactgtttccattctgtcgacaaacatgtcttccaaattttatcacaaacacttttgg 1680
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QY 1681 agggtaaaccaagttttattctgtaagaacaggggaacactatgttgctgcataatcct 1740
Db 26105 AGGTTAACCAAGTTGTTATTCGTAAGAAGAGGGGGAACCTATGTTGCTGCATAATCCT 26046
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QY 2941 gaatcaca 2948
Db 24845 GAATCACA 24838

RESULT 2
D50276
LOCUS D50276 4156 bp DNA PLN
DEFINITION Saccharomyces cerevisiae Hst1 gene, complete cds.
ACCESSION D50276
VERSION D50276.1 GI:1777313
KEYWORDS Hst1; high-copy suppressor of TFP sensitivity.
SOURCE Saccharomyces cerevisiae (strain:RAY-3A) DNA.
ORGANISM Saccharomyces cerevisiae
Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 4156)
Tsuchiya, E.
Direct Submission
Submitted (13-APR-1995) to the DDBJ/EMBL/GenBank databases. Eiko
Tsuchiya, Hiroshima University Faculty of Engineering, Department
of Fermentation Technology; Kagami-yama, Higashi-Hiroshima,
Hiroshima 739, Japan (E-mail:etsuchi@ipc.hiroshima-u.ac.jp,
Tel:0824-24-7868, Fax:0824-24-7868)
2 (bases 1 to 4156)
Tsuchiya, E., Matsuzaki, G., Tsukao, A. and Miyakawa, T.
Molecular cloning and characterization of S. cerevisiae Hst1 gene
Unpublished (1995)
3 (sites)
Tsuchiya, E., Matsuzaki, G., Kurano, K., Fukuchi, T., Tsukao, A. and
Miyakawa, T.
The Saccharomyces cerevisiae SSD1 gene is involved in the toll-like
to high concentration of Ca²⁺ with the participation of
HST1/NRCL/BFR1
Gene 176 (1-2), 35-38 (1996)
97075905
Location/Qualifiers
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/strain="RAY-3A"
/db_xref="taxon:4932"
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/codon_start=1
/protein_id="BAA08819.1"
/db_xref="GI:1816450"

TITLE
The Saccharomyces cerevisiae SSD1 gene is involved in the toll-like
to high concentration of Ca²⁺ with the participation of
HST1/NRCL/BFR1
JOURNAL
MEDLINE
FEATURES
source

gene
CDS
/standard_name="high-copy suppressor of TFP sensitivity"
/codon_start=1
/protein_id="BAA08819.1"
/db_xref="GI:1816450"

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NRGLSRHGNASLIRPSTLRSTEFDDNEDDDNKDGSASFTVKNVERISKIERPY
SLRDTITELTKINSAGLTDNDATILARTLSMAGSYSDKKDQPOPEGHDEGDFGST

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2002, 10:38:12 ; Search time 4622.84 Seconds
(without alignments)
6512.739 Million cell updates/sec

Title: US-09-165-460A-1

Perfect score: 1825

Sequence: 1 accctacacacacacacacacacatt 1825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenBank:

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_om.*
20: em_or.*
21: em_ov.*
22: em_pat.*
23: em_ph.*
24: em_pl.*
25: em_ro.*
26: em_sts.*
27: em_sy.*
28: em_un.*
29: em_vl.*
30: em_htgo_hum.*
31: em_htgo_inv.*
32: em_htgo_rod.*
33: em_htg_hum.*
34: em_htg_inv.*
35: em_htg_rod.*
36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	1823.4	99.9	1825	8	SCYJR117W	249617 S.cerevisia
2	1553.4	85.1	1706	8	SCYJR117W	077137 Saccharomyc
3	342	18.7	1555	8	SCYJR116W	249616 S.cerevisia
c 4	195	10.7	99360	8	NCH11N2	AL513444 Neurospor
5	187	10.2	36920	8	SPAC3H1	268144 S. pombe ch
6	137.2	7.5	1275	8	AF353722	AF353722 Arabidops
c 7	136	7.5	686	6	A86270	A86270 Sequence 92
c 8	136	7.5	686	6	ARI55763	ARI55763 Sequence
c 9	136	7.5	686	6	E66288	E66288 Genome DNA
10	121	6.6	935	8	SCYJR118C	249618 S.cerevisia
11	117.4	6.4	1859	9	AF064867	AF064867 Homo sapi
12	117.4	6.4	2963	9	AB016068	AB016068 Homo sapi
13	117.4	6.4	2966	9	HSY13834	Y13834 Homo sapien
14	117.4	6.4	2968	6	E32056	E32056 Human AFCl
15	114.2	6.3	1340	3	AF358443	AF358443 Physarum
16	98.4	5.4	78592	3	AC004335	AC004335 Drosophill
c 17	98.4	5.4	102413	2	AC020024	AC020024 Drosophill
c 18	92.8	5.1	41327	3	CBRG47J19	CBRG47J19
c 19	91.6	5.0	40767	3	CEC04F12	CEC04F12
c 20	88	4.8	317511	1	CJ1168X3	281461 Caenor. 1
21	86.6	4.7	582	8	AL139076	AL139076 Campyloba
22	81.6	4.5	660	8	CNS018PP	AL110644 Botrytis
23	72.2	4.0	2161	9	CNS01AH3	AL112927 Botrytis
24	66.8	3.7	1072	6	AX027874	AX027874 Homo sapi
c 25	66.6	3.6	124808	2	AP000652	AX055334 Sequence
c 26	65.6	3.6	16488	1	AE004992	AP000652 Homo sapi
27	65	3.6	256172	2	AC005139	AE004992 Halobacte
c 28	64.4	3.5	169423	2	AC069309	AC005139 Plasmodi
c 29	64.4	3.5	186306	2	AC083946	AC069309 Mus muscu
30	63.6	3.5	1245	6	AX055202	AC083946 Mus muscu
c 31	63.6	3.5	19715	1	AE000555	AX055202 Sequence
c 32	63.6	3.5	234112	3	PFMAL4P2	AE000555 Helicobac
33	62.4	3.4	13383	3	AE001374	AL035475 Plasmodi
c 34	61.8	3.4	98734	2	PFMAL1P2	AE001374 Plasmodi
35	61.6	3.4	14943	1	AE001528	AL031745 Plasmodi
36	59.8	3.3	12029	3	AE001392	AL049184 Plasmodi
37	59.8	3.3	110000	2	AC087899_0	AC074166 Mus muscu
c 38	59.2	3.2	114736	3	PFMAL3P3	AC087899 Mus muscu
39	59.2	3.2	253305	3	PFMAL3P7	298547 Plasmodi
40	58.8	3.2	98899	2	AL603743	AL034559 Plasmodi
41	58.8	3.2	318221	2	PFMAL13P3	AL603743 Denio rer
c 42	58.8	3.2	318503	2	AC074166	AL049184 Plasmodi
c 43	58.4	3.2	172239	2	AC069587	AC074166 Mus muscu
c 44	58.2	3.2	12029	3	AE001412	AC069587 Homo sapi
c 45	58.2	3.2	187469	9	AL357312	AE001412 Plasmodi
						AL357312 Human-HNA

ALIGNMENTS

RESULT 1
SCYJR117W

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

JOURNAL

TITLE

Direct Submission

Submitted (25-SEP-1995) Data collected by MIPS on behalf of the

European yeast chromosome X sequencing project. MIPS at the

Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152

SCYJR117W 1825 bp DNA PLN 11-AUG-1997
S.cerevisiae chromosome X reading frame ORF YJR117W.

249617 Y13136

249617.1 GI:1015836

baker's yeast.

Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

1 (bases 1 to 1825)

Rose, M., Koetter, P. and Entian, K.D.

Unpublished

2 (bases 1 to 1825)

MIPS.

Direct Submission

Submitted (25-SEP-1995) Data collected by MIPS on behalf of the

European yeast chromosome X sequencing project. MIPS at the

Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152

QY	331	aggccctttattcatgtttgatcttagacagattcttcgcacatccctaataatcccgtygaaa	390
DB	61	AGGCCCTTTATTTCATGTTTGATCTTAAGACGATTCTCGACCATCCCTANTATCCCGTGGAAA	120
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DB	121	TTAATCATTTCTGGGTTCCTCGATGGCCAAATTTCTTTGAAATCTTACTTGACGTACAGA	180
QY	451	cagtcaccagaagctatctgaacaaaggctgcacactgtctcggaaagagaattgatgat	510
DB	181	CAGTACCAGAAGCTATCTGAAACAAAGTTGCCACCTGTCTGGAAGAGCAAAATTTGATGAT	240
QY	511	gaacttttcaataaacaaggaaactactcccggggccaaagccaaagttcccattttccgt	570
DB	241	GAACAATTTTCATAAAACAAGAACTACTCCGGGCCAAGGCCAAGTTCTCCATTTTCGGT	300
QY	571	gacgtctataacctagcccaaaagctagttttcaataatnagacacctcttccctaaaatc	630
DB	301	GACGCTATTAACCTAGCCCAAAAGCTAGTTTTTCATCAAAATCGACCTCTTCCCTAAAATC	360
QY	631	tggcacatggccgtttctttattgaatcagtcctcggccagtcagatttcataatggtctcc	690
DB	361	TGGCACATGGCCGTTCTTTATGATGCGAGTCCTGCCACATCATTTATATGATGCTCC	420
QY	691	actgtgcacagaggttatgctctttgggtctcttaccagtttcttgcataccttggttgat	750
DB	421	ACTGTGCGACAGAGTTTATGCTTCTTGGGTCTCTTATCCACGTTGTCTACCTTGGTTGAT	480
QY	751	ttgcacctctctactatagccattttgctctgggaagaaaaattggttttcaatacaaatg	810
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DB	601	GGCCCCAATCCTTTACTCTGTTCCTTAAGATCTTTGATAAATCCCTACTGATTTCCTTGG	660
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DB	661	TACATTATGGTCTCTTGTGTCTCCAAATCTTAGCCATGACAATCATTCAGTCTTC	720
QY	991	atcgtgccatgtttaataaagttcaactccattggagcggtgaactgaaaaaatctatt	1050
DB	721	ATCATGCCCATGTTTAATAAGTTTCACCTCCATTGGAGGACCGTGAATGAAAAAATCTATT	780
QY	1051	gaaagtttggccgataagttgggttcccctctatagataaagatttttgaattgacggctca	1110
DB	781	GAAAGTTTGGCCGATAGAGTTGGGTTCCTCTAGATAAAGATTTTTCTCATTTGACGCTCA	840
QY	1111	aaaagatctctctattcaaacgcataattcaagggtttgccattccacctccaagaaatt	1170
DB	841	AAAAGATCTTCTCATTTCAACGCATATTTCCACAGGTTTGCCATTCACCTCCAAGAGAAAT	900
QY	1171	gtttgttcgcacctttagtgaaacagtaattctactgataagaaattacggctgttttgccc	1230
DB	901	GTTTTGTTCGACACTTTAGTGAACAGTAATTTCTACTGATGAATATACGGCTCTTTTGGCC	960
QY	1231	catgaatactgctactggcaaaaaaacacatcgtttaatatgtgtcatcttttagtcaattg	1290
DB	961	CATGAATTCGGTCTACTGGCAAAAAAACCATCGTTAATATGTGTCTATCTTTAGTCAATG	1020
QY	1291	cacaccttctctcatttctcccttttcacagcatctacagaaatacatcattttacaac	1350
DB	1021	CACACCTTCCTCATTTTCTCCCTTTTCACAGCATCTACAGAAATACATCATTTTACAAC	1080
QY	1351	acctcgggttttcttagaagaagtcacctggcgagtttgttgatcccggttatcacaaag	1410
DB	1081	ACCTTCGGCTTTTCTTAGAAGAGTCCACTGGCAGCTTTGTTGATCCCGTTATCACAAG	1440
QY	1411	gaattcccaattatcattggatttatgttatttaacgacttattaaactccactcgaaagt	1470